

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/382,088A

DATE: 05/01/2001
TIME: 08:39:08

Input Set : A:\12932-003001.TXT
Output Set: N:\CRF3\05012001\I382088A.raw

4 <110> APPLICANT: Hope, Ernest G.
5 Negrin, Robert
7 <120> TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PROTECTING
8 ORGANS, TISSUE AND CELLS FROM IMMUNE SYSTEM-MEDIATED DAMAGE
11 <130> FILE REFERENCE: 12932-003001
13 <140> CURRENT APPLICATION NUMBER: US 09/382,088A
14 <141> CURRENT FILING DATE: 1999-08-24
16 <150> PRIOR APPLICATION NUMBER: US 60/097,640
17 <151> PRIOR FILING DATE: 1998-08-24
19 <160> NUMBER OF SEQ ID NOS: 29
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 9
25 <212> TYPE: PRT
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: consensus sequence
31 <221> NAME/KEY: VARIANT
32 <222> LOCATION: 2
33 <223> OTHER INFORMATION: Xaa = Val, Leu, Ala, or Thr
35 <221> NAME/KEY: VARIANT
36 <222> LOCATION: 3
37 <223> OTHER INFORMATION: Xaa = Leu or His
39 <221> NAME/KEY: VARIANT
40 <222> LOCATION: 4
41 <223> OTHER INFORMATION: Xaa = Ser or Val
43 <221> NAME/KEY: VARIANT
44 <222> LOCATION: 6
45 <223> OTHER INFORMATION: Xaa = Asp or Glu
47 <221> NAME/KEY: VARIANT
48 <222> LOCATION: 7
49 <223> OTHER INFORMATION: Xaa = Gln, Lys, or Arg
51 <221> NAME/KEY: VARIANT
52 <222> LOCATION: (8)...(8)
53 <223> OTHER INFORMATION: Xaa = Leu or Val
55 <400> SEQUENCE: 1
56 Ala Xaa Xaa Xaa Ala Xaa Xaa Xaa Arg
57 1 5
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 9
61 <212> TYPE: PRT
62 <213> ORGANISM: Artificial Sequence
64 <220> FEATURE:
65 <223> OTHER INFORMATION: consensus sequence
67 <221> NAME/KEY: VARIANT
68 <222> LOCATION: 2
69 <223> OTHER INFORMATION: Xaa = Val or Ala

ENTERED

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71 <221> NAME/KEY: VARIANT
 72 <222> LOCATION: 3
 73 <223> OTHER INFORMATION: Xaa = Leu or His
 75 <221> NAME/KEY: VARIANT
 76 <222> LOCATION: 4
 77 <223> OTHER INFORMATION: Xaa = Ser or Val
 79 <400> SEQUENCE: 2
 80 Ala Xaa Xaa Xaa Ala Glu Gln Leu Arg
 81 1 5
 83 <210> SEQ ID NO: 3
 84 <211> LENGTH: 9
 85 <212> TYPE: PRT
 86 <213> ORGANISM: Homo sapiens
 88 <400> SEQUENCE: 3
 89 Ala Val Leu Ser Ala Glu Gln Leu Arg
 90 1 5
 92 <210> SEQ ID NO: 4
 93 <211> LENGTH: 1254
 94 <212> TYPE: DNA
 95 <213> ORGANISM: Homo sapiens
 97 <400> SEQUENCE: 4
 98 ctataactcg tctcgcatct tgtcaccctt gagccggacc aggcgccaa tgaatagcag 60
 99 ggagccgctt tgggtgtccc gcaccaggaa gatgaagggg tggtcggcgt agaacagctt 120
 100 ggggtgcgc agctcctcgc gcccgtagat gtcttggtca aagggttgcc catctgtgtc 180
 101 caactcaaag gcggtggcgt ggaacacact ggccaggtag agatccttct tgccagacat 240
 102 gcgtgataag tcggccttgt tcttgatcaat ggccctcagtc aggccagacc cagccagggtg 300
 103 tttctgcagg tcatgggtca cctccaccac acccttgggc aaggagatgg caacagcctt 360
 104 cttctgcacg ttcccatcc agatcttcag ctgctctttg gtttagcagct tttcaaggcg 420
 105 ctcgagaggc tccacgtgat ggggcatgag gatgatgagg ctggagagct tgtgagccag 480
 106 gggcatctcc accagctgca gcttctcctt ctgctcgtcg tagtagttgt agaggcctgt 540
 107 ccggtgcacg atcgtaacac ccacagtata ggaccgagtc accatgaagc cacggttgctc 600
 108 caccatcttg tggtggaatt tctcatccca gtgtggcttg aagaacatgg cgttgactag 660
 109 cagggcgccg tccgtgctct ccacgtcctt ggtgacctcg ggcagcttgc cgtcgggtgt 720
 110 ctgctcgccg cactcgttga tggactgcag cgcgctgcgc ttgtccggga agttgatctt 780
 111 ggagtgctcg cagttgtagt gctgcttgct gctcgccacg aagtcacag cgaagctcac 840
 112 tgagctgggt ccgtacagtc ggtgcccag cttccaggtc acgttgccg cgtcgagtt 900
 113 gctgagtgag cgcagcagct caccagggc ggcgtgcacc tcctcgtcgc gcagctgctc 960
 114 ggcgctcagc actgccttg cctgcgacgc cgtggtcgcc ttgccgccca gcgacacgag 1020
 115 acccagcgac gaggccacca ccacgggtga caccaggatg ttctccactg cctgggtcctt 1080
 116 ggccattgac tgatacaggc tgaaggccag gcctgtgctg ggctctgcca gtgtgggtcg 1140
 117 cttggaactc agcttctccg cagtaccagg ggctgcggcc tctacagggt tcttcacctc 1200
 118 ggctgccagg gccacagcca ggaggcataa ggtgcccgaga aggagagagc gcat 1254
 120 <210> SEQ ID NO: 5
 121 <211> LENGTH: 1254
 122 <212> TYPE: DNA
 123 <213> ORGANISM: Homo sapiens
 125 <220> FEATURE:
 126 <221> NAME/KEY: CDS
 127 <222> LOCATION: (1)...(1251)

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```

129 <400> SEQUENCE: 5
130 atg cgc tct ctc ctt ctg ggc acc tta tgc ctc ctg gct gtg gcc ctg      48
131 Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
132 1      5      10      15
134 gca gcc gag gtg aag aaa cct gta gag gcc gca gcc cct ggt act gcg      96
135 Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
136      20      25      30
138 gag aag ctg agt tcc aag gcg acc aca ctg gca gag ccc agc aca ggc      144
139 Glu Lys Leu Ser Ser Lys Ala Thr Thr Leu Ala Glu Pro Ser Thr Gly
140      35      40      45
142 ctg gcc ttc agc ctg tat cag gca atg gcc aag gac cag gca gtg gag      192
143 Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
144      50      55      60
146 aac atc ctg gtg tca ccc gtg gtg gtg gcc tcg tcg ctg ggt ctc gtg      240
147 Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val
148 65      70      75      80
150 tcg ctg ggc ggc aag gcg acc acg gcg tcg cag gcc aag gca gtg ctg      288
151 Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu
152      85      90      95
154 agc gcc gag cag ctg cgc gac gag gag gtg cac gcc ggc ctg ggt gag      336
155 Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu
156      100      105      110
158 ctg ctg cgc tca ctc agc aac tcg acg gcg cgc aac gtg acc tgg aag      384
159 Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys
160      115      120      125
162 ctg ggc agc cga ctg tac gga ccc agc tca gtg agc ttc gct gat gac      432
163 Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp
164      130      135      140
166 ttc gtg gcg agc agc aag cag cac tac aac tgc gag cac tcc aag atc      480
167 Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile
168 145      150      155      160
170 aac ttc ccg gac aag cgc agc gcg ctg cag tcc atc aac gag tgg gcc      528
171 Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala
172      165      170      175
174 gcg cag acc acc gac ggc aag ctg ccc gag gtc acc aag gac gtg gag      576
175 Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu
176      180      185      190
178 agc acg gac ggc gcc ctg cta gtc aac gcc atg ttc ttc aag cca cac      624
179 Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His
180      195      200      205
182 tgg gat gag aaa ttc cac cac aag atg gtg gac aac cgt ggc ttc atg      672
183 Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met
184      210      215      220
186 gtg act cgg tcc tat act gtg ggt gtt acg atg atg cac cgg aca ggc      720
187 Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly
188 225      230      235      240
190 ctc tac aac tac tac gac gac gag aag gag aag ctg cag ctg gtg gag      768
191 Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu
192      245      250      255

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```

194 atg ccc ctg gct cac aag ctc tcc agc ctc atc atc ctc atg ccc cat      816
195 Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His
196          260          265          270
198 cac gtg gag cct ctc gag cgc ctt gaa aag ctg cta acc aaa gag cag      864
199 His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln
200          275          280          285
202 ctg aag atc tgg atg ggg aag atg cag aag aag gct gtt gcc atc tcc      912
203 Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser
204          290          295          300
206 ttg ccc aag ggt gtg gtg gag gtg acc cat gac ctg cag aaa cac ctg      960
207 Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu
208 305          310          315          320
210 gct ggg ctg ggc ctg act gag gcc att gac aag aac aag gcc gac tta      1008
211 Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu
212          325          330          335
214 tca cgc atg tct ggc aag aag gat ctg tac ctg gcc agt gtg ttc cac      1056
215 Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His
216          340          345          350
218 gcc acc gcc ttt gag ttg gac aca gat ggc aac ccc ttt gac cag gac      1104
219 Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp
220          355          360          365
222 atc tac ggg cgc gag gag ctg cgc agc ccc aag ctg ttc tac gcc gac      1152
223 Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp
224          370          375          380
226 cac ccc ttc atc ttc ctg gtg cgg gac acc caa agc ggc tcc ctg cta      1200
227 His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu
228 385          390          395          400
230 ttc att ggg cgc ctg gtc cgg ctc aag ggt gac aag atg cga gac gag      1248
231 Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu
232          405          410          415
234 tta tag      1254
235 Leu
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 417
241 <212> TYPE: PRT
242 <213> ORGANISM: Homo sapiens
244 <400> SEQUENCE: 6
245 Met Arg Ser Leu Leu Leu Gly Thr Leu Cys Leu Leu Ala Val Ala Leu
246 1          5          10          15
247 Ala Ala Glu Val Lys Lys Pro Val Glu Ala Ala Ala Pro Gly Thr Ala
248          20          25          30
249 Glu Lys Leu Ser Ser Lys Ala Thr Thr Leu Ala Glu Pro Ser Thr Gly
250          35          40          45
251 Leu Ala Phe Ser Leu Tyr Gln Ala Met Ala Lys Asp Gln Ala Val Glu
252          50          55          60
253 Asn Ile Leu Val Ser Pro Val Val Val Ala Ser Ser Leu Gly Leu Val
254 65          70          75          80
255 Ser Leu Gly Gly Lys Ala Thr Thr Ala Ser Gln Ala Lys Ala Val Leu
256          85          90          95

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```

257 Ser Ala Glu Gln Leu Arg Asp Glu Glu Val His Ala Gly Leu Gly Glu
258      100      105      110
259 Leu Leu Arg Ser Leu Ser Asn Ser Thr Ala Arg Asn Val Thr Trp Lys
260      115      120      125
261 Leu Gly Ser Arg Leu Tyr Gly Pro Ser Ser Val Ser Phe Ala Asp Asp
262      130      135      140
263 Phe Val Ala Ser Ser Lys Gln His Tyr Asn Cys Glu His Ser Lys Ile
264 145      150      155      160
265 Asn Phe Pro Asp Lys Arg Ser Ala Leu Gln Ser Ile Asn Glu Trp Ala
266      165      170      175
267 Ala Gln Thr Thr Asp Gly Lys Leu Pro Glu Val Thr Lys Asp Val Glu
268      180      185      190
269 Ser Thr Asp Gly Ala Leu Leu Val Asn Ala Met Phe Phe Lys Pro His
270      195      200      205
271 Trp Asp Glu Lys Phe His His Lys Met Val Asp Asn Arg Gly Phe Met
272      210      215      220
273 Val Thr Arg Ser Tyr Thr Val Gly Val Thr Met Met His Arg Thr Gly
274 225      230      235      240
275 Leu Tyr Asn Tyr Tyr Asp Asp Glu Lys Glu Lys Leu Gln Leu Val Glu
276      245      250      255
277 Met Pro Leu Ala His Lys Leu Ser Ser Leu Ile Ile Leu Met Pro His
278      260      265      270
279 His Val Glu Pro Leu Glu Arg Leu Glu Lys Leu Leu Thr Lys Glu Gln
280      275      280      285
281 Leu Lys Ile Trp Met Gly Lys Met Gln Lys Lys Ala Val Ala Ile Ser
282      290      295      300
283 Leu Pro Lys Gly Val Val Glu Val Thr His Asp Leu Gln Lys His Leu
284 305      310      315      320
285 Ala Gly Leu Gly Leu Thr Glu Ala Ile Asp Lys Asn Lys Ala Asp Leu
286      325      330      335
287 Ser Arg Met Ser Gly Lys Lys Asp Leu Tyr Leu Ala Ser Val Phe His
288      340      345      350
289 Ala Thr Ala Phe Glu Leu Asp Thr Asp Gly Asn Pro Phe Asp Gln Asp
290      355      360      365
291 Ile Tyr Gly Arg Glu Glu Leu Arg Ser Pro Lys Leu Phe Tyr Ala Asp
292      370      375      380
293 His Pro Phe Ile Phe Leu Val Arg Asp Thr Gln Ser Gly Ser Leu Leu
294 385      390      395      400
295 Phe Ile Gly Arg Leu Val Arg Leu Lys Gly Asp Lys Met Arg Asp Glu
296      405      410      415
297 Leu
300 <210> SEQ ID NO: 7
301 <211> LENGTH: 9
302 <212> TYPE: PRT
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: synthetically generated peptide
308 <400> SEQUENCE: 7
309 Ala Ala His Val Ala Glu Gln Leu Arg

```

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:374 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:544 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:580 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29